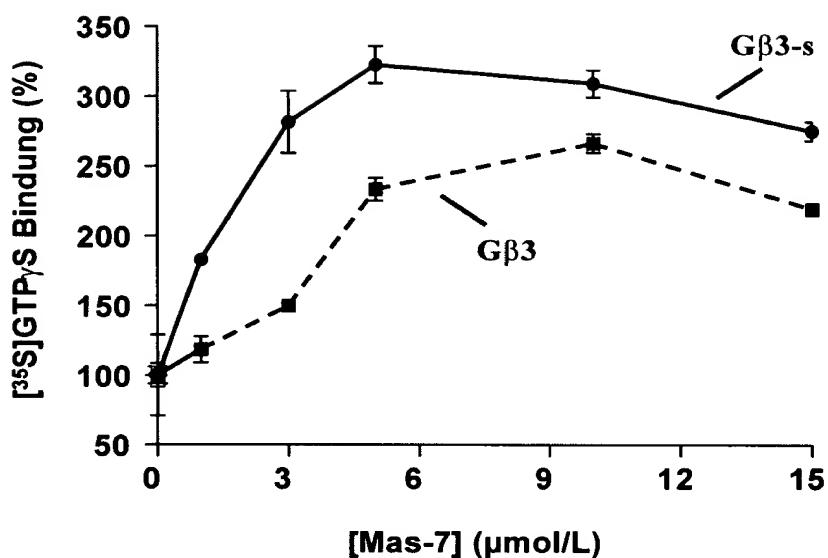


FIG. 1

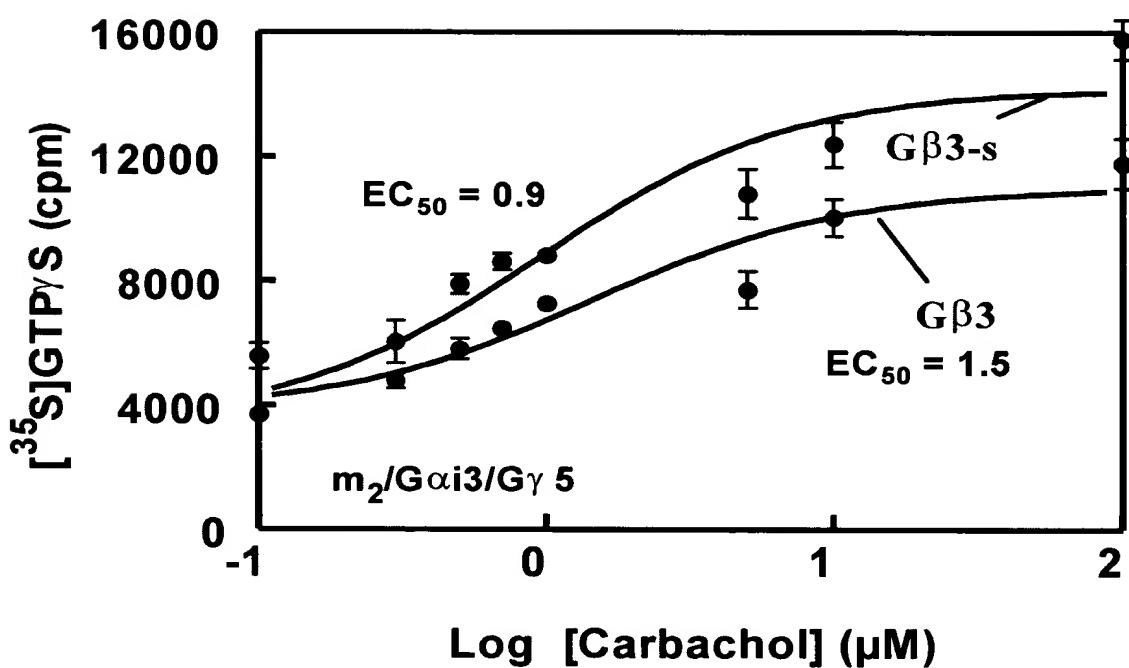


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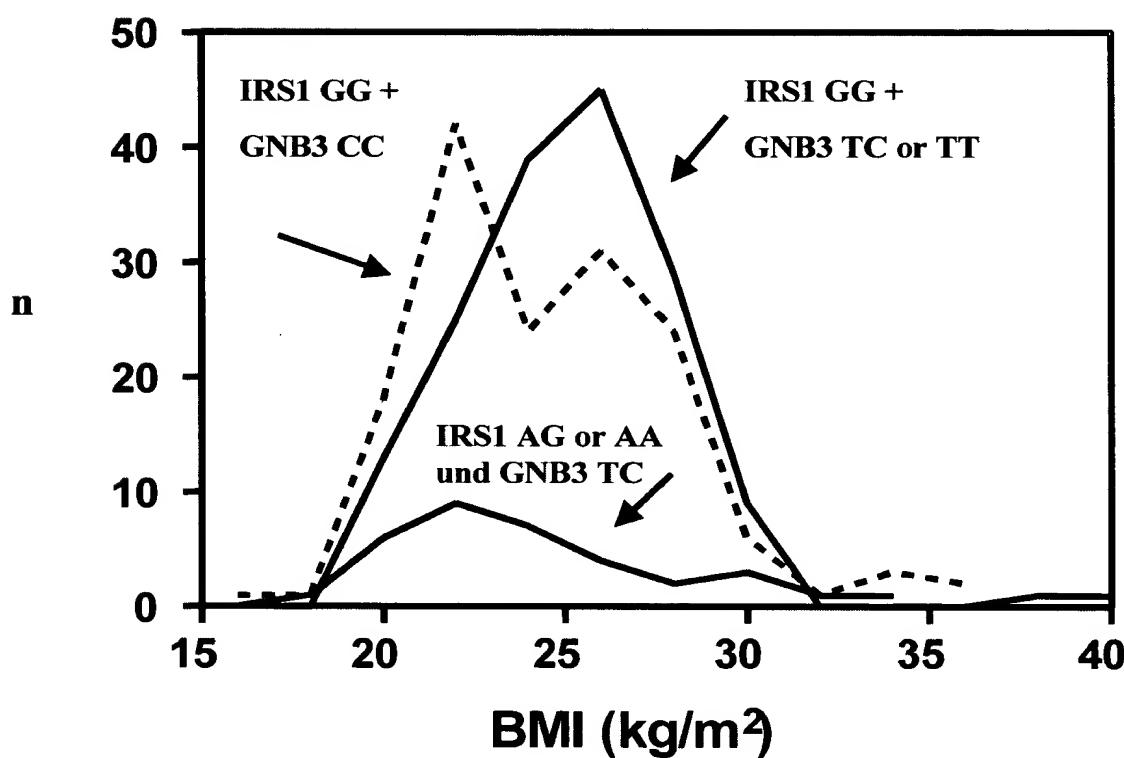
FIG. 2





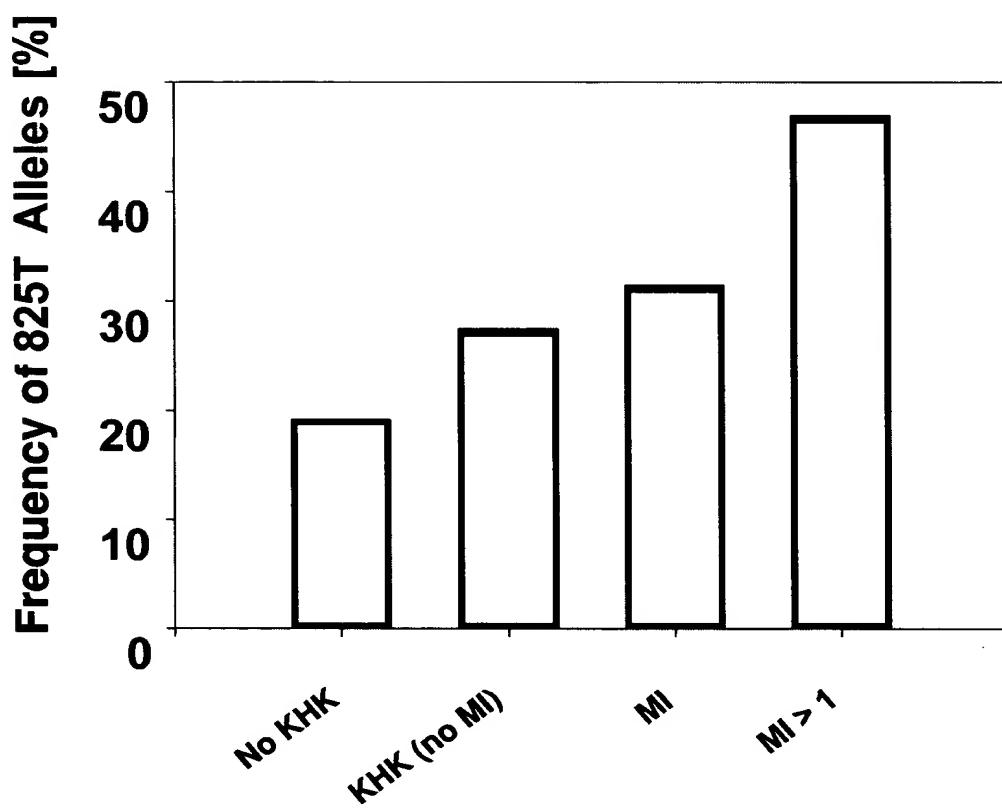
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FIG. 3



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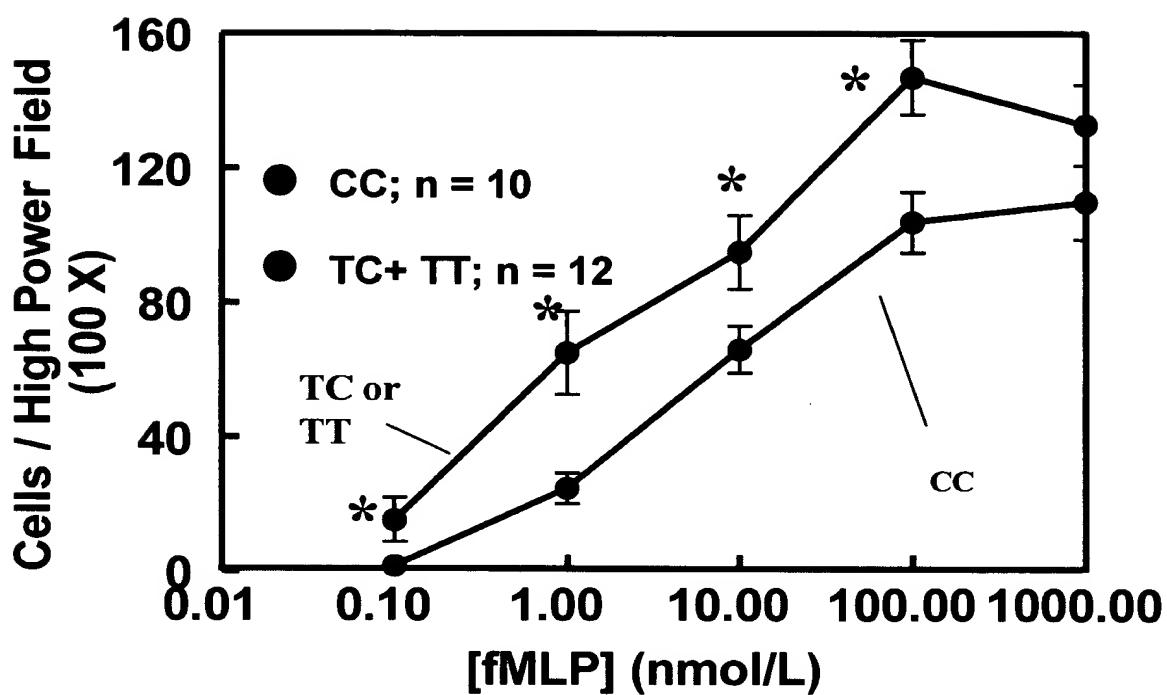
FIG. 4





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FIG. 5

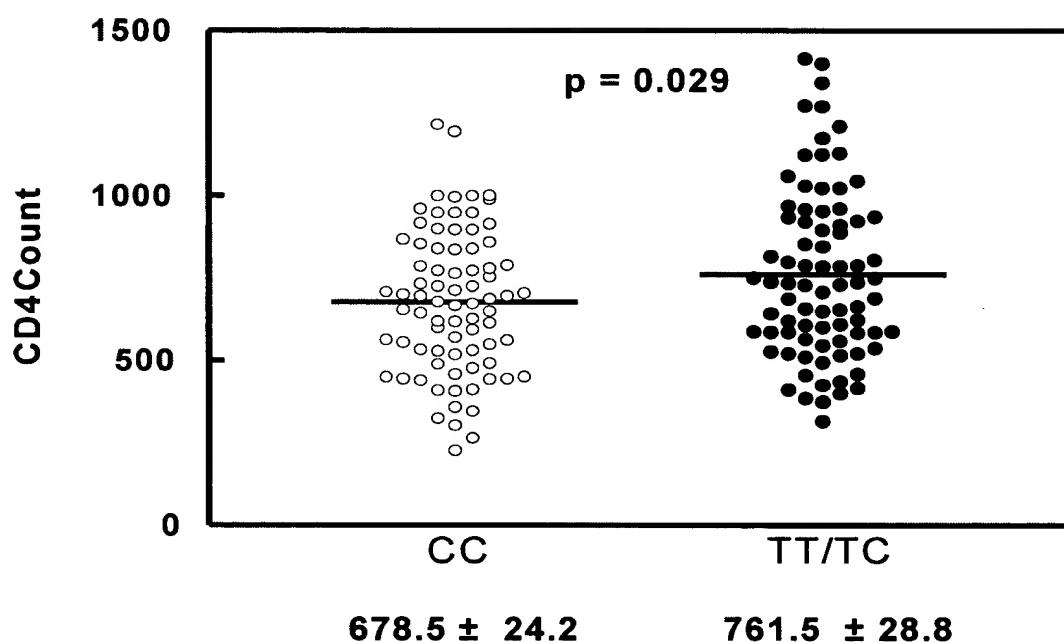


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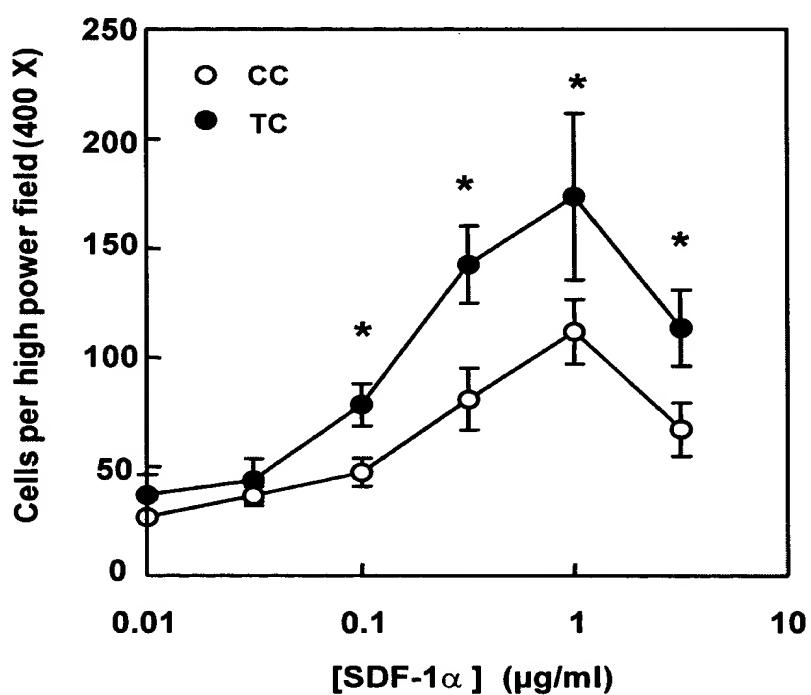
FIG. 6



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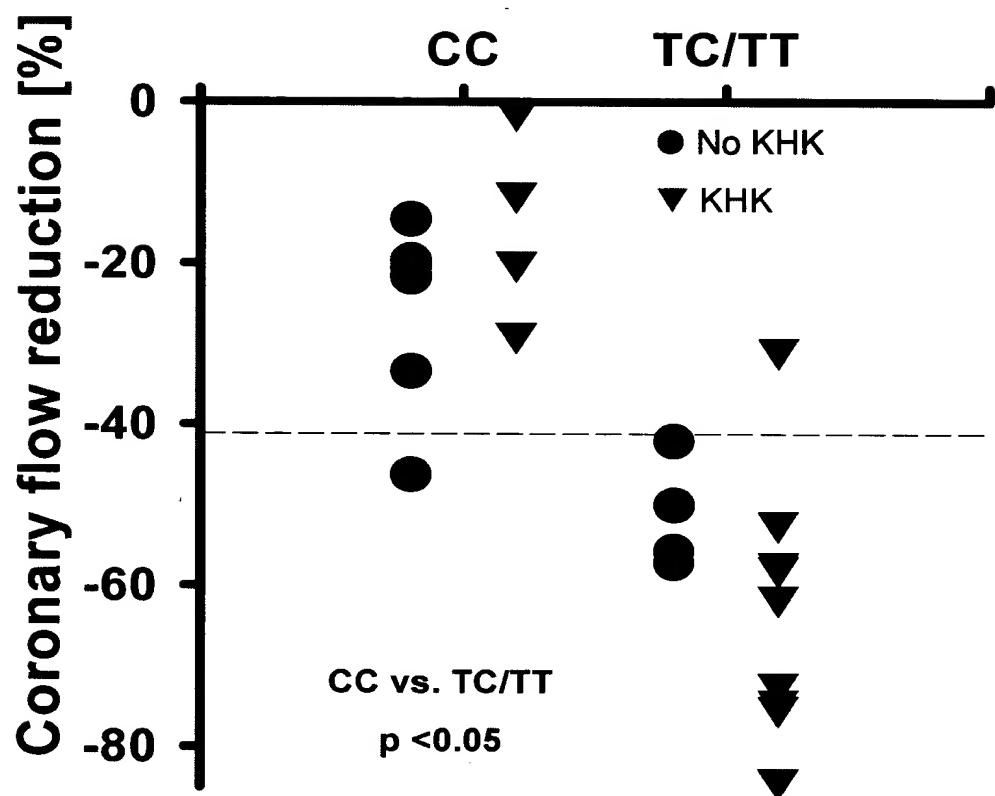
FIG. 7

**Enhanced Chemotaxis of T-Lymphocytes from
825T Allele Carriers**



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FIG. 8



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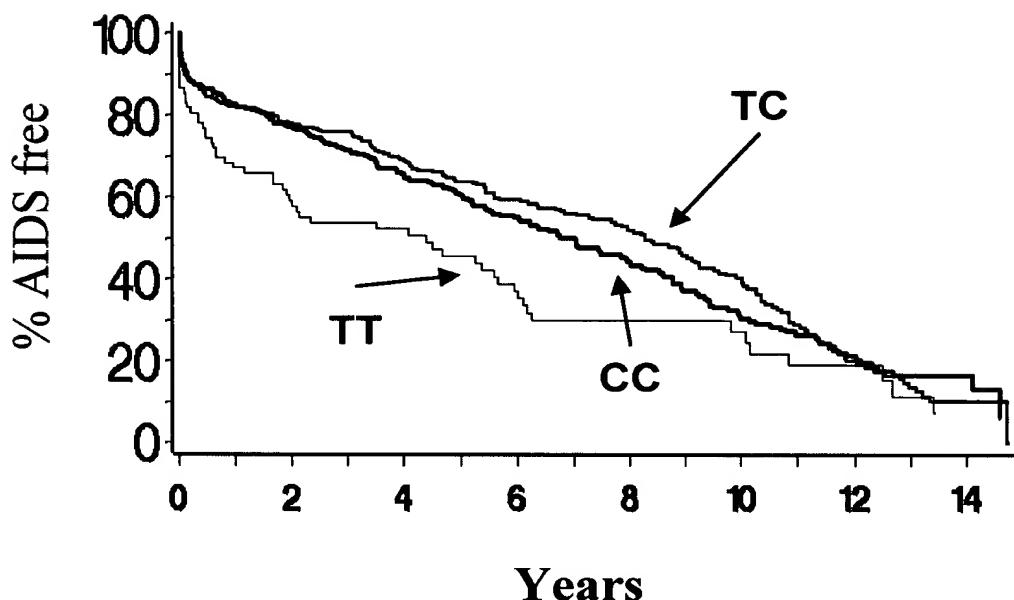
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FIG. 9

Time to AIDS

AIDS is defined as AIDS-defining disorders or CD4 count < 200

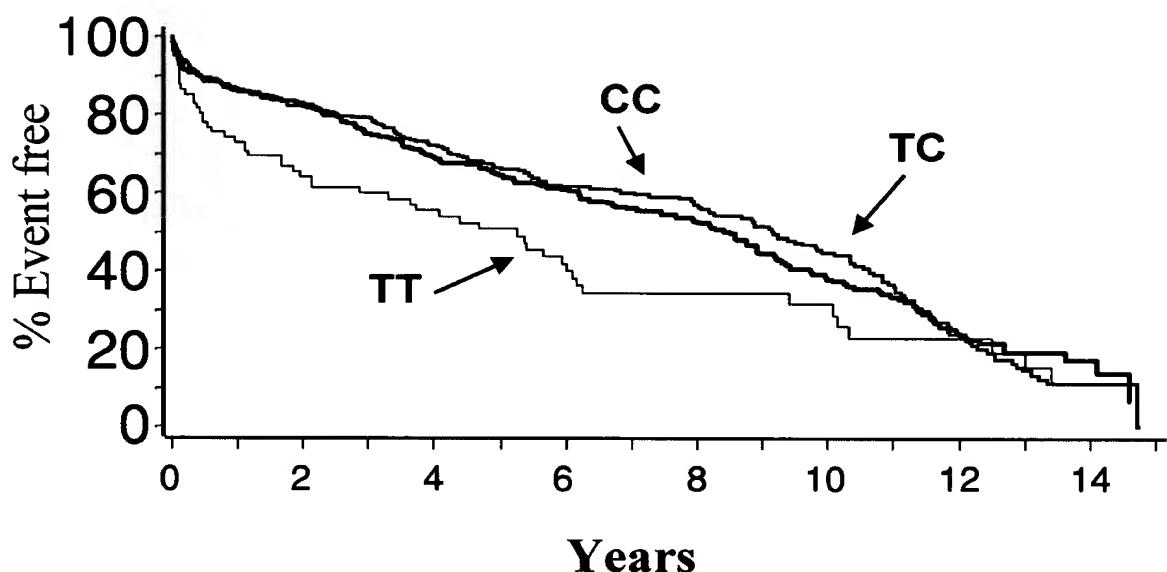




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FIG. 10

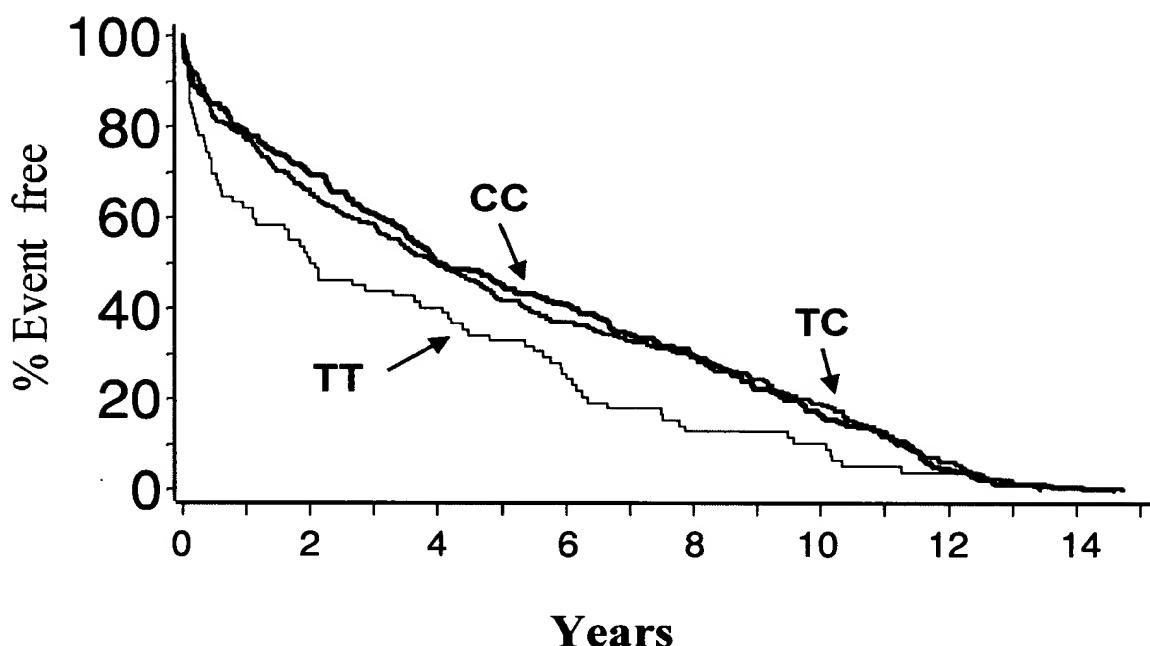
Event: CD4 Cell Count Below 200 per μ l



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FIG. 11

Event: Lowest CD4 Cell Count

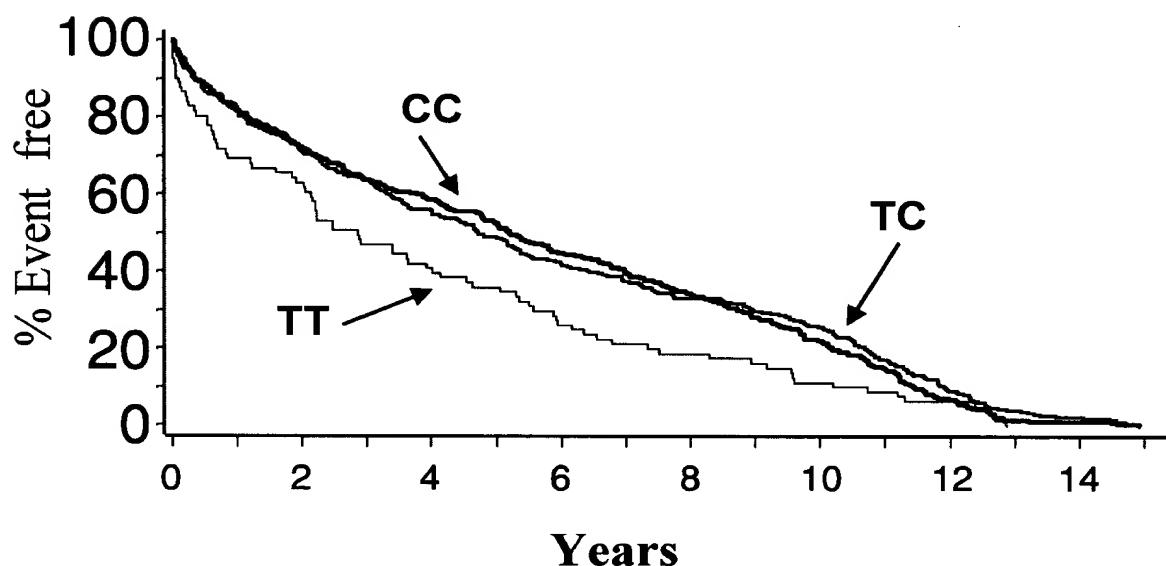


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FIG. 12

Event: Time to maximum HIV Virus Load

Virus Copy Number determined by Quantitative PCR

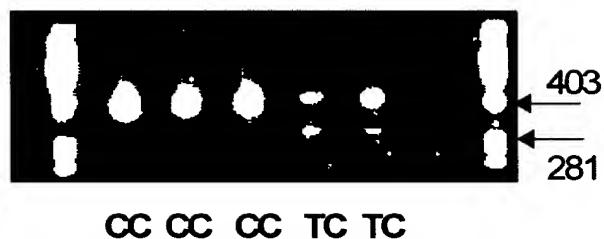




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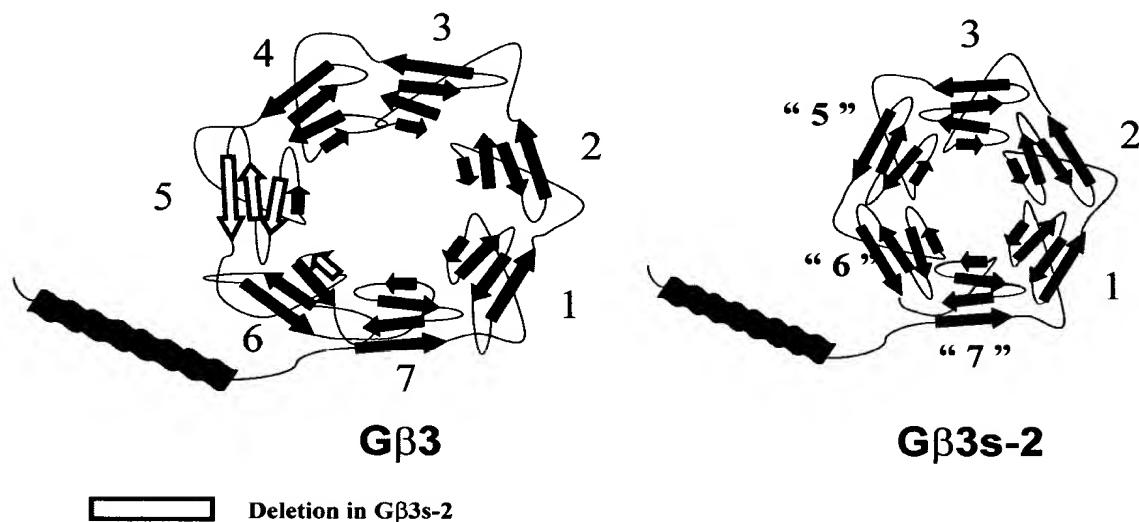
FIG. 13



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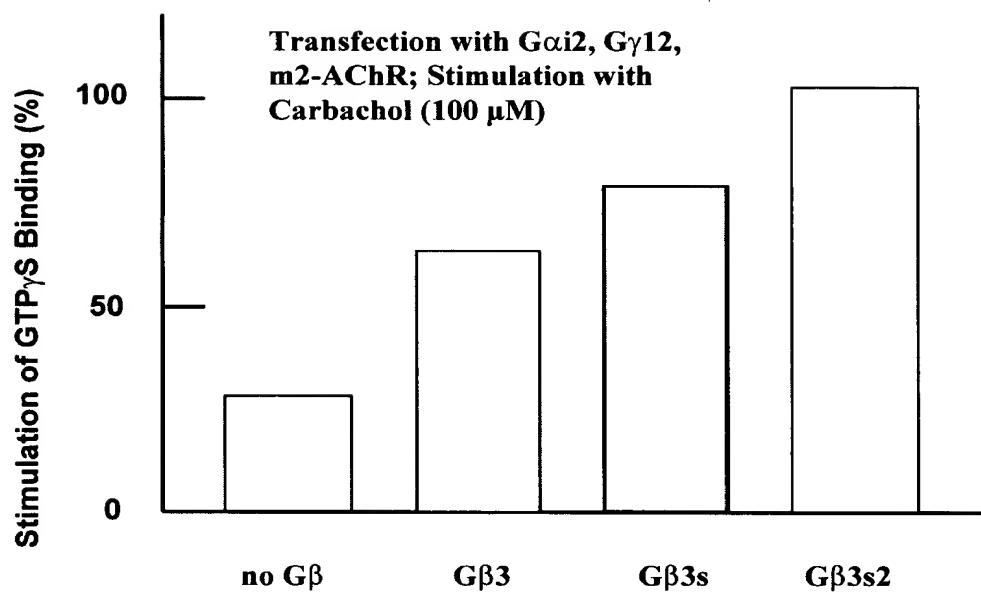
FIG. 14

Potential Structures of G β 3 and G β 3s / G β 3s-2



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FIG. 15



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FIG. 16

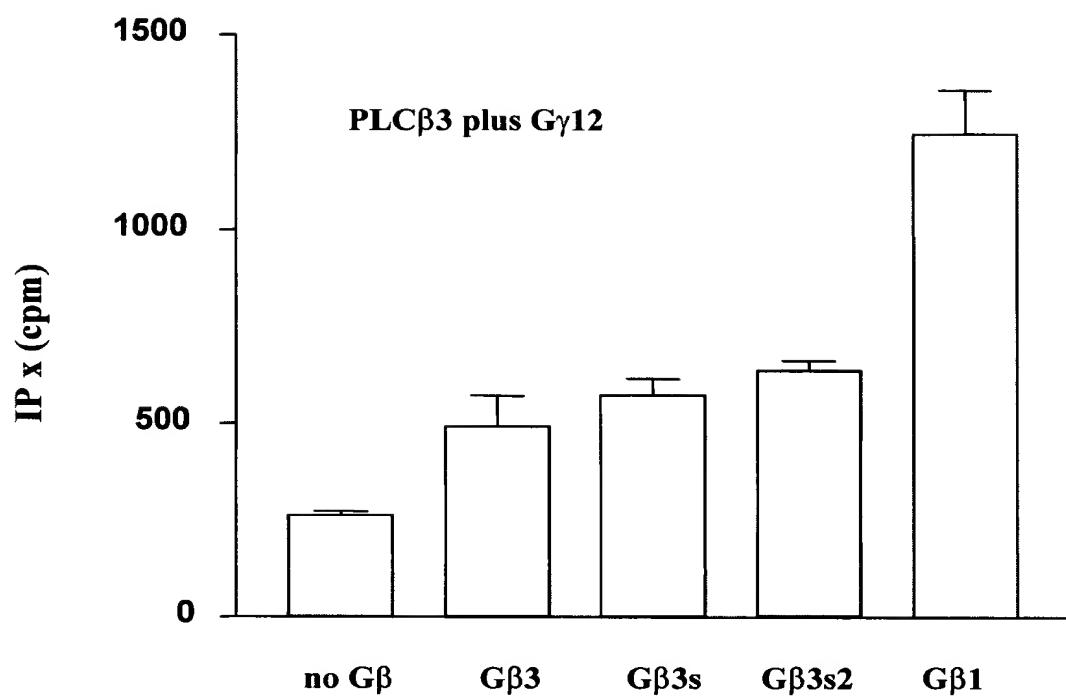




FIG. 17

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β 3-original sequence of Levine. The exons are underlined alternately. The area which is omitted by cryptic splice as bold-faced.

1 gggtcgATGG GGGAGATGGA GCAACTGCGT CAGGAAGCGG AGCAGCTAA GAAGCAGATT
Start-ATG EXON 3 after Ansari-Lari
Nucleotide 1-6 seem not to be affected

61 GCAGATGCCA GGAAAGCTG TGCTGACGTT ACTCTGGCAG **AGCTGGTGTC** TGGOCTAGAG
/Beginning EXON 4 /EXON 5 Beginning
=> ENDE 1 KLOM ANSARI

121 GTGGTGGGAC GAGTCCAGAT GOGGACGOGG CGGACGTTAA GGGGACACCT GGCCAAGATT
EXON 5

181 TACGCCATGC ACTGGGOCAC TGATTCTAAG CTGCTGGTAA GTGCCTCGCA AGATGGGAAG
EXON 5 / Beginning EXON 6

241 CTGATCGTGT GGGACAGCTA CACCACCAAC AAGGTGCACG CCATCCCAC GCGCTCCTCC
EXON 6 / EXON 7

301 TGGGTCATGA CCTGTGOCTA TGCCCCATCA GGGACTTTG TGGCATGTGG GGGGCTGGAC
EXON 7

361 AACATGTGTT CCATCTACAA CCTCAAATCC CGTGAGGGCA ATGTCAAGGT CAGCGGGAG
EXON 7

421 CTTTCTGCTC ACACAGGTTA TCTCTCCTGC TGCCGCTTCC TGGATGACAA CAATATTGTG
EXON 7 /EXON 8

481 ACCAGCTCGG GGGACACCAC GTGTGCCTTG TGGACATTG AGACTGGCA GCAGAAGACT
EXON 8 /EXON 9
cryptic SPlicing

541 GTATTTGTGG GACACACGGG TGACTGCATG AGCCTGGCTG TGTCTCCTGA CTTCAATCTC
EXON 9
cryptic SPlicing

601 TTCATTTCGG GGGCTGTGA TGCCAGTGCC AAGCTCTGGG ATGTGCGAGA GGGGACTGC
EXON 9
cryptic SPlicing /

661 CGTCAGACTT TCACTGGOCA CGAGTCGGAC ATCAACGCCA TCTGTTCTT CCCAAATGGA
EXON 9 / Beginning EXON 10

721 GAGGGCCATCT GCACGGGCTC GGATGACGCT TOCTGCGGCT TGTTGACCT GGGGGCAGAC
EXON 10



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FIG. 17(cont.)

781 CAGGAGCTGA TCTGCTTCTC CCACGAGAGC ATCATCTGCG GCATCACGTC CGTGGCCTTC
EXON 10 Polymorphism site acgtc tgt

841 TCCCTCAGTG GCGGCCTACT ATTGCTGGC TAOGACGACT TCAACTGCAA TGTCTGGGAC
EXON 10

901 TCCATGAAGT CTGAGCGTGT GGGCATCCTC TCTGCCACG ATAACAGGGT GAGCTGCCTG
EXON 10 /Beginning EXON 11

961 GGAGTCACAG CTGACGGGAT GGCTGTGGCC ACAGGTTCTT GGGACAGCTT CCTAAAATC
EXON 11

1021 TGGAACTGAg gaggctggag aaagggaagt ggaaggcagt gaacacactc aqcgcccc
EXON 11
End of Open Reading Frame

1081 tgcggccatcc catctcattc aggtgttctc ttctatattc cgggtgccat tcccactaa
EXON 11

1141 ctttctcctt tgagggcagt ggggagcatg ggactgtgcc tttgggaggc agcatcaggg
EXON 11

1201 acacaggggc aaagaactgc cccatctcctt cccatggcct tccctccccca cagtcctcac
EXON 11

1261 agcctctccc ttaatgagca aggacaacctt gcccctcccc agccctttgc aggcccagca
EXON 11

1321 gacttgagtc tgaggccccca ggcccttagga ttccctccccca agagccacta cctttgtcca
EXON 11

"Ban Polymorphismus"
tctggcacta cta

1381 ggccctgggtg gtataggccg tttggccctg tgactatgac tctggcacca cttagggtcc
EXON 11

1441 ggccctcttc ttattcatgc tttctccttt ttctaccctt ttttctctcc taagacacct
EXON 11

1501 gcaataaaagt gtagcaccct ggt
EXON 11 POLY A SITE



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FIG. 18

Sequence with two polymorphisms (Numbering after the Levine sequence)

gggtogatgg	gaggagatgga	gcactcggt	caggagogg	agacgtcaa	gaagcagatt	60
gcagatgoca	ggaaagactg	tgcgtgaogtt	actctggcag	agctgggtgc	tggcttagag	120
gtggtgtggac	gagtocagat	oggaoogogg	oggaotgtaa	ggggacact	ggcaagatt	180
taogocatgc	actgggocac	tgatttctaag	ctgctgtttaa	gtgctogca	agatggaaag	240
ctgatogtgt	gggacagctt	caacaacaac	aagggtcaog	ccatccact	gogctoctoc	300
tgggtcatga	octgtgocta	tgcocatca	ggaaactttt	tggcatgtgg	ggggctggac	360
aacatgtgtt	ccatctacaa	ccctaaatoc	cggtgggca	atgtcaagg	cagcgggag	420
ctttctgctc	acacaggitta	tctctoctgc	tgcgccttcc	tggatgacaa	caatattgtg	480
accagctogg	gggacaocac	gtgtgocttg	tggcacattt	agactggca	gcagaagact	540
gtatttgtgg	gacacaoggg	tgactgcatg	agccctggctg	tgtctoctga	cttcatactc	600
ttcatttogg	gggcctgtga	tgcagtgcc	aaacctctgg	atgtgggaga	ggggacactgc	660
ogtcagactt	tcaactggcca	cgaggatggac	atcaacgoca	tctgtttctt	ccccaatgga	720
gaggocatct	gcacgggctc	ggatgaoct	tccatggcgt	tgttttgcct	ggggcagac	780
caggagctga	tctgtttctc	ccaaagagac	atcatctgog	gcacatcgtc	tgtggcttc	840
toocctagtg	gcggactact	atccatgtgc	taacgtact	tcaactgcaa	tgtctggac	900
tocatgaagt	ctgaggttgt	gggcatoctc	tctggcaog	ataacaggt	gagctgoctg	960
ggagttcacag	ctgacgggat	ggctgtggcc	acagggttct	ggacacgtt	ccctaaatcc	1020
tggaaactgag	gaggctggag	aaaggaaat	ggaggcagt	gaacacactc	agcagcccc	1080
tgcacggacoc	catctctattc	agggtttctc	ttcttatattc	ogggtgcatt	toocactaag	1140
ctttctcttt	tgagggcagt	ggggagcatg	ggactgtgc	tttggggaggc	agcatcagg	1200
acacaggccc	aaagaactgc	ccatctctt	ccatggcct	toocctccaa	cagtctcac	1260
agccctctcc	ttaatgagca	aggacaaccc	gcacccccc	agccctttgc	aggcccac	1320
gacttgagtc	tgaggcccca	ggcccttagga	ttccctccccc	agagccacta	ccctttgtca	1380
tctggacta	ctagggctgg	gtggatagg	gggtttggcc	ctgtgactat	ggctctggca	1440
ccacttaggt	octggccctc	ttcttattca	tgccttcctcc	tttttttctcc	tttttttctcc	1500
toctaagaca	octgcaataa	agtgtacac	ctgtgtt			1536



FIG. 19

Nucleic acid sequence of cDNA of G β 3 and description of the deletion in G β 3 and G β 3s-2. Numbering referenced to the cDNA of Levine et al. (Levine, M.A., Smallwood, P.M., Moen, P.T., Jr., Helman, L.J., and Ahn, T.G. Molecular cloning of β 3 subunit, a third form of the G protein beta-subunit polypeptide. *Proc.Natl.Acad.Sci.USA* 87(6):2329-2333, 1990) Here numbering does not begin with start codon ATG, but 6 nucleotides earlier in the 5' area.

1 gggtcgATGG GGGAGATGGA GCAACTGCGT CAGGAAGCGG AGCAGCTCAA GAAGCAGATT
Start-ATG EXON 3
Nucleotide 1-6 seem not to be affected

61 GCAGATGCGA GGAAAGCCTG TGCTGACGTT ACTCTGGCAG AGCTGGTGTC TGGCTAGAG
/Beginn EXON 4 /EXON 5 Beginning

121 GTGGTGGGAC GAGTCCAGAT GCGGACGCCGG CGGACGTTAA GGGGACACCT GGCCAAGATT
EXON 5

181 TACGOCATGC ACTGGGCCAC TGATTCTAAG CTGCTGGTAA GTGCCTCGCA AGATGGGAAG
EXON 5 / Beginning EXON 6

241 CTGATCGTGT GGGACAGCTA CACCACCAAC AAGGTGCACG CCATCCCACT GCGCTCCTCC
EXON 6 / EXON 7

301 TGGGTCATGA CCTGTGCTA TGCCCCATCA GGGAACTTTG TGGCATGTGG GGGGCTGGAC
EXON 7

361 AACATGTGTT CCATCTACAA CCTCAAATCC CGTGAGGGCA ATGTCAAGGT CAGCOGGGAG
EXON 7

421 CTTCTGCTC ACACAGGTTA TCTCTCCTGC TGCGCTTCC TGGATGACAA CAATATTGTG
EXON 7 /EXON 8 *Deletion bei G3s*

481 ACCAGCTCGG GGGACACCAC GTGTGCCCTTG TGGGACATTG AGACTGGGCA GCAGAAGACT
EXON 8 /EXON 9

541 GTATTTGTGG GACACACGGG TGACTGCATG AGCCTGGCTG TGTCTCCTGA CTTCAATCTC
EXON 9

601 TTCATTTCGG GGGCCTGTGA TGCCAGTGCC AAGCTCTGGG ATGTGCGAGA GGGGACCTGC
EXON 9 *Deletion in G3s2*

661 CGTCAGACTT TCACTGGCCA CGAGTCGGAC ATCAACGCCA TCTGTTCTT CCCCAATGGA
EXON 9 / Beginn EXON 10
Intron dazwischen 1607 bp



FIG. 19(cont.)

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Deletion in G3s2

721 GAGGCCATCT GCACGGGCTC GGATGACGCT TCCTGCCGCT TGTTTGACCT GCGGGCAGAC
EXON 10

781 CAGGAGCTGA TCTGCTTCTC CCACGAGAGC ATCATCTGCG GCATCACGTC CGTGGCCTTC
EXON 10 polymorphism site agtc tgt

841 TCOCTCAGTG GCGCGCTACT ATTGCTGGC TACGAOGACT TCAACTGCAA TGTCTGGGAC
EXON 10

901 TCCATGAAGT CTGAGCGTGT GGGCATCCTC TCTGGCCACG ATAACAGGGT GAGCTGCCTG
EXON 10 /Beginning EXON 11 (Intron dazw. 989 bp)

961 GGAGTCACAG CTGAOGGGAT GGCTGTGGCC ACAGGTTCT GGGACAGCTT CCTAAAATC
EXON 11

1021 TGGAACCTGAg gaggctggag aaaggagaat ggaaggcagt gaacacactc agcagccccc
EXON 11
End of Open Reading Frame B3-3

1081 tgcggaccc catctcattc aggtgttctc ttctatattc cgggtgccat tcccactaag
EXON 11

1141 ctttctccct tgagggcagt ggggagcatg ggactgtgcc tttgggaggc agcatcaggg
EXON 11

1201 acacaggggc aaagaactgc cccatctcct cccatggcct tccctcccc cagtcctcac
EXON 11

1261 agcctctccc ttaatgagca aggacaacct gcccctcccc agccctttgc aggcccagca
EXON 11

1321 gacttgagtc tgaggccccca ggcccttagga ttccctcccc agagccacta cctttgtcca
EXON 11

C1423T

1381 ggcctgggtq gtatagggcg tttggccctg tgactatggc tctggcadca cttagggtcct
EXON 11

1441 ggccctcttc ttattcatgc tttctccctt ttctaccttt ttttctctcc taagacacct
EXON 11

1501 gcaataaaagt gtagcaccct ggt
EXON 11 POLY A SITE



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FIG. 20

Amino acid sequence of Gβ3s-2 (Combined production)

atg ggg gag atg gag caa ctg cgt cag gaa ggc gag cag ctc aag aag	48	
Met Gly Met Glu Gln Leu Arg Gln Glu Ala Glu Gln Leu Lys Lys		
5	10	15
cag att gca gat gcc agg aaa gcc tgt gct gac gtt act ctg gca gag	96	
Gln Ile Ala Asp Ala Arg Lys Ala Cys Ala Asp Val Thr Leu Ala Glu		
20	25	30
ctg gtg tct ggc cta gag gtg gtg gga cga gtc cag atg cgg acg cgg	144	
Leu Val Ser Gly Leu Glu Val Val Gly Arg Val Gln Met Arg Thr Arg		
35	40	45
cgg acg tta agg gga cac ctg gcc aag att tac gcc atg cac tgg gcc	192	
Arg Thr Leu Arg Gly His Leu Ala Lys Ile Tyr Ala Met His Trp Ala		
50	55	60
act gat tct aag ctg ctg gta agt gcc tcg caa gat ggg aag ctg atc	240	
Thr Asp Ser Lys Leu Leu Val Ser Ala Ser Gln Asp Gly Lys Leu Ile		
65	70	75
gtg tgg gac agc tac acc acc aac aag gtg cac gcc atc cca ctg cgc	288	
Val Trp Asp Ser Tyr Thr Thr Asn Lys Val His Ala Ile Pro Leu Arg		
80	85	90
tcc tcc tgg gtc atg acc tgt gcc tat gcc cca tca ggg aac ttt gtg	336	
Ser Ser Trp Val Met Thr Cys Ala Tyr Ala Pro Ser Gly Asn Phe Val		
95	100	105
gca tgt ggg ggg ctg gac aac atg tgt tcc atc tac aac ctc aaa tcc	384	
Ala Cys Gly Gly Leu Asp Asn Met Cys Ser Ile Tyr Asn Leu Lys Ser		
110	115	120
cgt gag ggc aat gtc aag gtc agc cgg gag ctt tct gct cac aca ggt	432	
Arg Glu Gly Asn Val Lys Val Ser Arg Glu Leu Ser Ala His Thr Gly		
125	130	135
tat ctc tcc tgc tgc cgc ttc ctg gat gac aac aat att gtg acc agc	480	
Tyr Leu Ser Cys Cys Arg Phe Leu Asp Asp Asn Asn Ile Val Thr Ser		
140	145	150
155		



FIG. 20(cont.)

tcg ggg gac acc acg tgt gcc ttg tgg gac att gag act ggg cag cag 528
Ser Gly Asp Thr Thr Cys Ala Leu Trp Asp Ile Glu Thr Gly Gln Gln
160 165 170 175

aag act gta ttt gtg gga cac acg ggt gac tgc atg agc ctg gct gtg 576
Lys Thr Val Phe Val Gly His Thr Gly Asp Cys Met Ser Leu Ala Val
180 185 190

tct cct gac ttc aat ctc ttc att tcg ggg gcc tgt gat gcc agt gcc 624
ser Pro Asp Phe Asn Leu Phe Ile Ser Gly Ala Cys Asp Ala Ser Ala
195 200 205

aag ctc tgg gat gtg cga gag ggg acc tgc cgt cag act ttc act ggc 672
Lys Leu Trp Asp Val Arg Glu Gly Thr Cys Arg Gln Thr Phe Thr Gly
210 215 220

cag gag tcg gac atc aac gcc atc tgt ttc ttc tcc ctc agt ggc cgc 720
His Glu Ser Asp Ile Asn Ala Ile Cys Phe Phe Ser Leu Ser Gly Arg
225 230 235

ctt ctt ttc gct ggc tac gac gac ttc aac tgc aat gtc tgg gac tcc 768
Leu Leu Phe Ala Gly Tyr Asp Asp Phe Asn Cys Asn Val Trp Asp Ser
240 245 250 255

atg aag tct gag cgt gtg ggc atc ctc tct ggc cac gat aac agg gtg 816
Met Lys Ser Glu Arg Val Gly Ile Leu Ser Gly His Asp Asn Arg Val
260 265 270

agc tgc ctg gga gtc aca gct gac ggg atg gct gtg gcc aca ggt tcc 864
Ser Cys Leu Gly Val Thr Ala Asp Gly Met Ala Val Ala Thr Gly Ser
275 280 285

tgg gac agc ttc ctc aaa atc tgg aac tga 894
Trp Asp Ser Phe Leu Lys Ile Trp Asn ***
290 295